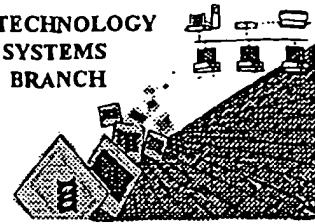


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/922,240
Source: IFW16
Date Processed by STIC: 7/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 08/922,240

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not saved** in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is **saved** in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa **can only represent** a single residue. Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading).
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
→ Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" **can only represent** a single nucleotide; "Xaa" **can only represent** a single amino acid



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/922,240

DATE: 07/23/2004
TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT
Output Set: N:\CRF4\07232004\H922240.raw

4 <110> APPLICANT: Schreiber, Stuart L.
5 Belshaw, Peter
6 Crabtree, Gerald R.
8 <120> TITLE OF INVENTION: GENE THERAPY BY CELL SPECIFIC TARGETING
11 <130> FILE REFERENCE: APBI-P01-007
13 <140> CURRENT APPLICATION NUMBER: US 08/922,240
14 <141> CURRENT FILING DATE: 1997-08-27
16 <150> PRIOR APPLICATION NUMBER: US 60/024,666
17 <151> PRIOR FILING DATE: 1996-08-27
19 <160> NUMBER OF SEQ ID NOS: 3
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 10
25 <212> TYPE: PRT
26 <213> ORGANISM: Unknown
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Peptide
W--> 31 <221> NAME/KEY: VARIANT
32 <222> LOCATION: 1
33 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid
W--> 35 <221> VARIANT
36 <222> LOCATION: 2
37 <223> OTHER INFORMATION: Xaa = Sar: sarcosine
W--> 39 <221> VARIANT
40 <222> LOCATION: 3, 5, 8, 9
41 <223> OTHER INFORMATION: Xaa = MeLeu: N-methylleucine
W--> 43 <221> VARIANT
44 <222> LOCATION: 7
45 <223> OTHER INFORMATION: Xaa = D-Ala: D-alanine
W--> 47 <221> VARIANT
48 <222> LOCATION: 10
49 <223> OTHER INFORMATION: Xaa = Ac-N-MeValinol ester
W--> 51 <400> 1
W--> 52 Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa Xaa
53 1 5 10
56 <210> SEQ ID NO: 2
57 <211> LENGTH: 12
58 <212> TYPE: PRT
59 <213> ORGANISM: Unknown
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Peptide
W--> 64 <221> NAME/KEY: VARIANT
65 <222> LOCATION: 1

pp1-3
Ques. 1. Simply
Ques. 2. 'Unknown'
Ques. 3. 'Unknown'

Understood - please attempt to give
source of genetic
material as explanation
for (213) Unknown
(see item 1 on
Error Summary
Sheet)

same error

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/922,240

DATE: 07/23/2004

TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT
 Output Set: N:\CRF4\07232004\H922240.raw

66 <223> OTHER INFORMATION: Xaa = Fmoc-CpSar:
 67 9-fluorenylmethoxycarbonyl-cyclopentyl sarcosine
 W--> 69 <221> VARIANT
 70 <222> LOCATION: 2
 71 <223> OTHER INFORMATION: Xaa = MeBmt:
 72 (4R)-N-methyl-4-butenyl-4-methyl-L-threonine
 W--> 74 <221> VARIANT
 75 <222> LOCATION: 3
 76 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid
 W--> 78 <221> VARIANT
 79 <222> LOCATION: 4
 80 <223> OTHER INFORMATION: Xaa = Sar: sarcosine
 W--> 82 <221> VARIANT
 83 <222> LOCATION: 5, 7, 10, 11
 84 <223> OTHER INFORMATION: Xaa = MeLeu: N-methylleucine
 W--> 86 <221> VARIANT
 87 <222> LOCATION: (9)...(9)
 88 <223> OTHER INFORMATION: Xaa = D-Ala: D-alanine
 W--> 90 <221> VARIANT
 91 <222> LOCATION: (12)...(12)
 92 <223> OTHER INFORMATION: Xaa = Valinol ester
 W--> 94 <400> 2
 W--> 95 Xaa Xaa Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa Xaa
 96 1 5 10
 99 <210> SEQ ID NO: 3
 100 <211> LENGTH: 11
 101 <212> TYPE: PRT
 102 <213> ORGANISM: Unknown
 104 <220> FEATURE:
 105 <223> OTHER INFORMATION: Peptide
 W--> 107 <221> NAME/KEY: VARIANT
 108 <222> LOCATION: 1
 109 <223> OTHER INFORMATION: Xaa = Me-CpSar: methyl-cyclopentyl sarcosine
 W--> 111 <221> VARIANT
 112 <222> LOCATION: 2
 113 <223> OTHER INFORMATION: Xaa = MeBmt:
 114 (4R)-N-methyl-4-butenyl-4-methyl-L-threonine
 W--> 116 <221> VARIANT
 117 <222> LOCATION: 3
 118 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid
 W--> 120 <221> VARIANT
 121 <222> LOCATION: 4
 122 <223> OTHER INFORMATION: Xaa = Sar: sarcosine
 W--> 124 <221> VARIANT
 125 <222> LOCATION: 5, 7, 10
 126 <223> OTHER INFORMATION: Xaa = MeLeu: N-methylleucine
 W--> 128 <221> VARIANT
 129 <222> LOCATION: (11)...(11)
 130 <223> OTHER INFORMATION: Xaa = MeLeu-(OH): hydroxyl-N-methylleucine

what about Xaa
 at location 9?
 (see p.3)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/922,240

DATE: 07/23/2004
TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT
Output Set: N:\CRF4\07232004\H922240.raw

W--> 132 <400> 3
W--> 133 Xaa Xaa Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa
134 1 5 10



RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/23/2004
PATENT APPLICATION: US/08/922,240 TIME: 13:24:43

Input Set : A:\APBI-P01-007.TXT
Output Set: N:\CRF4\07232004\H922240.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,2,3,5,7,8,9,10
 Seq#:2; Xaa Pos. 1,2,3,4,5,7,8,10,11,12
 Seq#:3; Xaa Pos. 1,2,3,4,5,7,9,10,11

VERIFICATION SUMMARY
PATENT APPLICATION: US/08/922,240

DATE: 07/23/2004
TIME: 13:24:43

Input Set : A:\APBI-P01-007.TXT
Output Set: N:\CRF4\07232004\H922240.raw

L:31 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:35 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:64 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:69 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:74 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:78 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:82 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:86 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:94 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:107 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:111 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:116 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:120 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:124 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:128 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:132 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0